

BEST AVAILABLE COPY

us-09-758-493-1_copy_1_188.rag

Tue Nov 15 15:32:23 2005

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2005, 17:04:13 ; Search time 163 Seconds

(without alignments)

446,075 Million cell updates/sec

Title: US-09-758-493-1_COPY 1_188

Perfect score: 965

Sequence: 1 CPOEDSDIAPNGSGSSTIP... YPQRNNEALKTQNQRK 188

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 2105692 seqs, 186760381 residues

Total number of hits satisfying chosen parameters: 1413077

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04;

1: geneseqp1980s;*

2: geneseqp1990s;*

3: geneseqp2000s;*

4: geneseqp2001s;*

5: geneseqp2002s;*

6: geneseqp2003s;*

7: geneseqp2004s;*

8: geneseqp2005s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	960	99.5	187	2	AY21991	Aay21991; Human com
2	893	92.5	177	5	AYU7686	Aau7686; Human int
3	890	92.1	177	5	AYU7685	Aau7685; Human int
4	534	55.3	187	2	AYY1922	Aayy1922; Human com
5	323	53.5	176	5	ABP78816	Abb78816; Von Willebrand factor CD1
6	286	53.5	176	5	AYY2349	Aayy2349; Human CD1
7	286	53.5	184	3	AYY2349	Aayy2349; Human CD1
8	286	53.5	184	6	ADG3895	Adg3895; Human exp
9	286	53.5	184	8	ADR03370	Adr03370; Human CD1
10	286	53.5	187	8	ADR23224	Adr23224; Human int
11	282	52.5	180	5	ABP76376	Abb76376; Lymphocyte
12	281.5	52.9	184	3	AYY23510	Aayy23510; Rhesus CD
13	281.5	52.9	184	8	ADG3896	Adg3896; Monkey CD
14	281.5	52.9	184	8	ADR03371	Adr03371; Rhesus macaque
15	276.5	29.7	184	5	AAU76848	Aau76848; Human int
16	276.5	29.7	184	5	AAU76857	Aau76857; Human int
17	262	27.2	181	4	ABU22614	Abu22614; Cell etru
18	231	23.9	178	3	AAB08817	Aab08817; A von Willebrand factor CD1
19	192.5	19.9	180	5	ABP4907	Abb4907; Von Willebrand factor CD1
20	171	17.7	33	2	AAR0392	Aar0392; Beta-2 integrin
21	171	17.7	33	2	AAW02044	Aaw02044; Human bet
22	171	17.7	116	7	ABW5598	Abw5598; Mouse pro
23	162.5	16.8	180	6	AAE32503	Aae32503; Mouse von Willebrand factor
24	160.5	16.6	180	6	AAE32500	Aae32500; Human von Willebrand factor
25	155.5	16.1	160	3	ABO8036	Aab08036; A von Willebrand factor

RESULT 1
AY21991
ID AY21991 standard; protein; 187 AA.
XX
AC AY21991;
XX
DR 13-SEP-1999 (first entry)
XX
DS Human complement factor MAC-1 vWF domain sequence.
XX
XX Factor B analogue; modified; complement activity; complement factor B;
KW consenus repeat domain; von Willebrand Factor domain; human; C;
KW CR3; autoimmune response; tissue damage; lupus erythematosus; therapy;
KW rheumatoid arthritis; hemolytic anemia; myasthenia gravis; injury; MAC-1;
KW myocardial infarction; acute shock lung syndrome; inflammation; vWF;
XX
OS Homo sapiens.
XX
PN USS928892-A.
XX
XX
PD 27-JUL-1999.
XX
PP 26-JUL-1996; 96US-00687706.
XX
PR 03-JAN-1994; 94US-00177109.
XX
PA (UNIV WASHINGTON,
Oglebay TV, Hourcade DR,
PI 1999-429498/36.
XX
PR Nucleic acids encoding complement protein homologues useful for
modulating function of the complement system in the treatment of a
variety of immune and autoimmune complex mediated syndromes.
XX
DR Disclosure; Fig 5a-B; 53pp; English.
XX
CC The invention relates to a Factor B Analogue that exhibits modified
complement activity in vitro. The analogue is generated by substituting a
short consensus repeat domain (SCR) or a von Willebrand Factor domain
(vWF) of human factor B with a SCR or a vWF from a second protein such as
human C2 or C3. The analogues may be used to regulate the complement
system involved in immune and autoimmune responses. Complement activity
can account for substantial tissue damage in a wide variety of autoimmune
immune complex mediated syndromes such as lupus erythematosus,
rheumatoid arthritis, hemolytic anemias and myasthenia gravis. Inhibition
of the complement system using the analogues is likely to provide a means

CC of therapeutic intervention in these cases. Inhibition of complement may
 CC also be favorable in cases that involve tissue damage caused by vascular
 CC injury such as myocardial infarction, cerebral vascular accidents or
 CC acute shock lung syndrome. In these cases the complement system may
 CC contribute to the destruction of partially damaged tissue. As in
 CC target specific antibodies could reduce the activity of tissue damaging
 CC proteins sites of inflammation. Complement inhibition is important in
 CC the present of xenograft rejection (the inhibition of complement by
 CC cell associated and soluble inhibitors is useful in protecting the
 CC transplant from damage caused by activation of endogenous complement. The
 CC present sequence represents the vifR domain of human factor Mac-1
 XX

Sequence 187 AA:

Query Match 99.5%; Score 960; DB 2; Length 187;
 Best Local Similarity 100.0%; Pred. No. 1.4e-97; Matches 187; Conservative 0; Indels 0; Gaps 0;
 Matches 187; Conservative 0; Mismatches 0;

Qy 1 CPQDSIAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60
 Db 1 CPQDSIAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60
 Db 61 BFOQNPNPISLVPKPTOLLRTHATGKVRVBLENTNGARNAKFLVLTUGKFG 120
 Qy 61 BFOQNPNPISLVPKPTOLLRTHATGKVRVBLENTNGARNAKFLVLTUGKFG 120
 Db 61 BFOQNPNPISLVPKPTOLLRTHATGKVRVBLENTNGARNAKFLVLTUGKFG 120
 Qy 121 DPGYESVTPAEDRGTVRYIGVDAFREKSRQLANTIASKEPDHYFQVNNEFAKT 180
 Db 121 DPGYESVTPAEDRGTVRYIGVDAFREKSRQLANTIASKEPDHYFQVNNEFAKT 180
 Qy 181 IONOLRE 187
 Db 181 IONOLRE 187

RESULT 2
 AAU76866 standard; protein; 177 AA.
 ID AAU76866;
 AC AAU76865;
 DT 21-MAY-2002 (first entry)
 XX Human integrin alpha subunit CD1b deletion variant A domain #2.
 KW Human; integrin alpha subunit; A domain; CD1b; integrin beta subunit;
 KW A-like domain; inflammatory disorder; skeletal muscle injury; resensitization;
 KW ischaemic reperfusion injury; immune complex; parasitic disease; mutant;
 KW antiinflammatory; vasotropic; antiparasitic; viliopathy; gene therapy;
 XX mutant.

OS Homo sapiens.
 Synthetic.

XX Location/Qualifiers

EH Key
 PT Misc-difference 172 "Wild-type Val substituted by Cys"
 PT Misc-difference 177 "Wild-type Ala substituted by Cys"

PT /note= "Wild-type Ala substituted by Cys"
 XX WO200209737-A1.

XX 07-FEB-2002.
 DD 31-JUL-2001; 2001WO-US023957.

XX Location/Qualifiers

EH Key
 PT Misc-difference 170 "note= "Wild-type Phe substituted by Cys"
 PT Misc-difference 177 "note= "Wild-type Ala substituted by Cys"

PT /note= "Wild-type Ala substituted by Cys"
 XX WO200209737-A1.

P1 Arnaut AM, Li R, Xiong J;
 XX WPI: 2002-188667/24.

DR Novel high affinity integrin polypeptide useful for treating restenosis
 XX and parasitic diseases. Comprises all or part of variant integrin alpha
 PT subunit A domain or variant integrin beta subunit A-like domain.

XX Claim 21; Page: 55pp; English.

PS The invention relates to a high affinity integrin polypeptide comprising
 XX all or part of a variant integrin alpha subunit A domain or a variant
 CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC integrin beta subunit A-like domain where Lys residue 312 has been replaced by
 CC G or A, at residue 313 and A at residue 310 have been replaced by C, or
 CC V at residue 315 and A at residue 310 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD1b or for treating inflammatory disorder; by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, for treating disorders caused by ischaemia-
 CC reperfusion injury, immune complex, parasitic diseases,
 CC two-hybrid or three-hybrid assays. This sequence represents a human
 CC integrin alpha subunit CD1b deletion variant A domain. Note: This
 CC variant sequence is not featured in the specification but has been
 XX derived from the wild-type protein shown in AAU76847.

SO Sequence 187 AA:

Query Match 92.5%; Score 893; DB 5; Length 177;

Best Local Similarity 100.0%; Pred. No. 3.4e-90; Matches 172; Conservative 2; Indels 0; Gaps 0;

Matches 172; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Qy 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGLIPHDPRMKPSTYMSOLKSKTILPSLMQYSEPRHPTPK 60

Db 1 CPQBDSDAPIFLDGSGL

AC	ABB78816;	xx	Sequence 176 AA;
DT	29-JUL-2002 (First entry)	SQ	Query Match 34.6%; Score 333.5; DB 5; Length 176;
DS	Von Willebrand factor type A domain protein SEQ ID NO:38.	xx	Best Local Similarity 43.4%; Pre. No. 2.8e-28; Matches 29;
XX	Human; NOX; cytosolic; antiarteriosclerotic; cardiovascular; lymphoma; anticidiabetic; immunosuppressive; neuroprotective; gene therapy; cancer; cardiomopathy; atherosclerotic; cell signal processing; diabetes; AIDS; metabolic pathway modulation; neoplastic; neurological disorders; asthma; adenocarcinoma; prostate cancer; uterus cancer; immune response; Crohn's disease; multiple sclerosis; Graft versus host disease.	xx	Wimberches 9, Indale 9, Cape 4;
RW	OS Unidentified.	xx	7 DIAPLODOSSTIPDPRMPEFYSYMMOLK- KSKTLESLMOSSEFRHTPTEKEFON 64
PN	WO2002010974-A2.	Oy	1 DIVFLDOSSTGQNFEVDPTPVERFLDIDPVYLVQSDBVRVREPKLQDN 60
PD	18-APR-2002.	Db	65 NNPPLSVAKPIKOL- LGRTHATCIRKORELFTNNGAKRKAQKILUVTTDKERKGDPD 123
PP	12-OCT-2001; 2001WO-US031922.	Qy	66 61 KOBVQDAKRIQYGGAGTNGTALQVRAFLTEAQSREGASQAPKVLTGDRSGDPD 120
XX	PR 12-OCT-2000; 2000US-0201113P.	Db	67 QY2DVTIPADRGESVYKYGDFDPSBKGSRQBLNTASKPRODYFVNPNPBLATION 183
PR	16-OCT-2000; 2000US-0200635P.	Qy	124 GRYDVIPADRGESVYKYGDFDPSBKGSRQBLNTASKPRODYFVNPNPBLATION 183
PR	16-OCT-2000; 2000US-0200637P.	PN	121 -- RDVNLNEKKAGVNPALGVNADNVB--- EUREIAKRPQHVFVSDPEALDQI 174
PR	16-OCT-2000; 2000US-0200648P.	PD	184 QL 195
PR	16-OCT-2000; 2000US-0200649P.	PP	175 LL 176
PR	16-OCT-2000; 2000US-0200652P.	RESULT 6	
PR	16-OCT-2000; 2000US-0200659P.	ID	AAV82349 standard; protein; 184 AA.
PR	16-OCT-2000; 2000US-0200701P.	XX	
PR	16-OCT-2000; 2000US-0200722P.	XX	
PR	16-OCT-2000; 2000US-021190P.	XX	
PR	18-JAN-2001; 2001US-0262455P.	XX	
XX	(CUDRA-) CURAGEN CORP. (MILL.) MILLET I.	DE	Human CD11a I-domain amino acid sequence SEQ ID NO:7.
PA	Grosse WM, Alisbrook JP, Lepley DM, Burgess CB, Mishra V; Shimada M, Shimaoka TD, Zarutian BD, Spytek KA; Edinger S, Gerlach V, Nadgouali J, Stone D, Gunther B, Silberman K; WPI: 2002 44117247.	DE	Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant; antitumour; antiviral; inflammatory function associated with gene 1; sepsis; arthritis; rhinitis; eczema; inflammatory bowel disease; systemic lupus erythematosus; leukaemia; viral infection; transplant rejection; graft rejection.
PT	New NOX polypeptides and polynucleotides, useful for treating or preventing a NOX-associated disorder or a pathological state in a subject, particularly a human, e.g. cardiomyopathy, atherosclerosis, cancer or diabetes.	XX	Homo sapiens.
PT	xx	OS	
PT	xx	PN	US6037454-A.
PT	xx	PD	14-MAR-2000.
PT	xx	PP	14-MAR-2000.
PS	Disclosure; Page 62; 227pp; English.	XX	XX
PS	xx	PP	20-NOV-1997; 97US-00974899.
CC	The present invention describes novel human proteins designated NOX (where X is 1, 2a, 2b, 2c, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOX1 is a tyrosine-protein kinase 6-like protein; NOX2 are keratin 4-like proteins; NOX3 is a collagen-like protein; NOX4 is a cystatin B-like protein; NOX5 is a serotonin receptor-like protein; NOX6 and NOX65 are cold inducible glycoprotein 30-like proteins; NOX7 is a matrixin-2-like protein; NOX8 is a leukocyte surface antigen (CD53)-like protein; and NOX9 is a tyrosine kinase-like protein. NOX sequences have cytotoxic, antiarrestoclerotic, cardiovascular, antidiabetic, immunosuppressive and nucroprotective activities, and can be used in gene therapy. The NOX sequences can be used in therapeutic applications particularly for treating, preventing or alleviating a NOX-associated disorder or a pathological state in a subject, particularly a human. These disorders include cardiomopathy, atherosclerosis, a disorder related to cell signal processing and metabolic pathway modulation or diabetes. The NOX sequences are also useful for determining the presence of or NOX predisposition to a disease associated with altered levels of NOX peptidopeptide or nucleic acid, particularly cancer. The NOX sequences are especially useful in therapeutic or prophylactic applications for neoplastic or neurological disorders, and in the treatment of adenocarcinoma, lymphoma, prostate cancer, uterous cancer, immune response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft versus host disease. The present sequence represents a von Willebrand factor type A domain protein sequence which is given in a domain analysis comparison with the human NOV7 protein from the present invention	XX	Example; Fig 2; 38pp; English.
CC	xx	XX	The present invention describes a humanised anti-CD11a antibody (Ab) that binds specifically to the human CD11a I-domain. The Ab has anti-inflammatory, immunosuppressive, antitumour and antiviral activities. The Ab blocks lymphocyte function-associated antigen (LFA-1) which is involved in leucocyte adhesion associated with inflammatory and immunological responses. The Ab are used (i) orally when coupled to a cyclophilin, to treat or prevent disorders caused by lymphocyte activation-associated antigen-1 (LFA-1, CD11a/CD18), e.g., septic shock, inflammatory bowel disease, eczema, systemic lupus erythematosus, rhinitis, leukaemia, viral infections, and many others, also for inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for

PR 20-NOV-1997; 97US-00974899.
 PR 20-OCT-1997; 99US-00412075.
 XX (GSTH) GENENTECH INC.
 XX Jardieu PM, Preete LG;
 WPI; 2004-051511/05.
 XX Humanized anti-CD1a antibody useful for treating lymphocyte function-associated antigen mediated disorder e.g. psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
 PS Example: SEQ ID NO 7; 45pp; English.
 PT The invention relates to a Humanised anti-cluster of differentiation (CD)1a antibody having specificity to human CD1a I-domain or CD1a with a kd value of not more than 1X10⁻⁸ M, or concentration for 50% inhibition (IC50) value of not more than 1 nM in mixed lymphocyte epidermal keratinocytes expressing intercellular adhesion molecule (ICAM 1). Also included are a kit comprising the antibody and instructions for use to detect the CD1a protein, an isolated nucleic acid encoding the antibody, a vector comprising the nucleic acid, a host cell comprising the vector and producing the antibody by culturing the cell so that the antibody is expressed. The antibody binds to epitope MH24 on CD1a. The antibody is useful for determining the presence of CD1a protein and for treating lymphocyte function associated antigen 1 mediated disorder such as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis and diabetes mellitus. The antibody is useful when conjugated to a producing activating enzyme, or as an affinity purification agent. The present sequence is the Human CD1a I-domain, the target for the antibody of the invention.
 XX Sequence 164 AA;
 SQ Query Match 29 7%; Score 286.5; DB 8; Length 184;
 Best Local Similarity 33.5%; Prd No. 4.7e-21;
 Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;
 Qy 7 DPAFDGSSSIIPDPFRKKEFVSTWHEQLKSKTFLSMOYSEBRPHPFKEPQNNP 66
 Db 5 DPAFDGSSSIIPDPFRKKEFVSTWHEQLKSKTFLSMOYSEBRPHPFKEPQNNP 64
 Qy 67 NPSLIVKPTDQIIGHTATGIRKVRDFPNTNGARQPKILWVUTDSEKGCPDLYE 126
 Db 65 DDALLKXHMLLNPFGAINTVATPFRBLGARDPATVLLITID--ATDSGNI 122
 Qy 127 DYPDADEREGVITYRIGYGDAPSRSKPSRBLNTASPRDVFQVNTPALYDQR 186
 Db 123 DAQD----IIRYIGIGKHPQTKEQQTUHKPASPBPVILDFKLDLFTEQ 177
 Qy 187 EK 188
 Db 178 KK 179

XX Location/Qualifiers
 FH Key Region 3..11 /note= "Beta strand 1"
 PT Region 19..34 /note= "Alpha helix 1"
 PT Region 39..53 /note= "Alpha helix 1"
 PT Region 57..62 /note= "Beta strand 2"
 PT Region 67..71 /note= "Alpha helix 2"
 PT Region 92..93 /note= "Alpha helix 3"
 PT Region 105..112 /note= "Alpha helix 4"
 PT Region 122..126 /note= "Beta strand 3"
 PT Region 139..145 /note= "Alpha helix 5"
 PT Region 142..151 /note= "Beta strand 4"
 PT Region 160..163 /note= "Alpha helix 6"
 PT Region 167..178 /note= "Beta strand 5"
 PT Region XX /note= "Alpha helix 7"
 PN US2004146507-A1.

XX PD 29-JUL-2004.
 XX PP 03-DEC-2003; 2003US-00727737.
 XX PR 27-NOV-1996;
 PR 20-NOV-1997;
 PR 97US-0031945P.
 XX (GSTH) GENENTECH INC.
 XX DR WPI; 2004-552640/53.
 XX PT New antibody mutant of a species-dependent antibody, useful for treating infectious diseases, especially inflammatory bowel disease, allergic conditions, autoimmune diseases, or cancer.
 XX DR Example: SEQ ID NO 7; 5pp; English.
 XX CC The present invention relates to an antibody mutant of a species-dependent antibody with beneficial properties. The invention is useful for treating and preventing infectious diseases such as human immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin disease such as psoriasis, inflammatory bowel diseases such as Crohn's disease and ulcerative colitis, adult respiratory distress syndrome, CC allergic diseases such as eczema and asthma, autoimmune diseases such as rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes mellitus, Reynaud's syndrome, immunological diseases such as tuberculous sarcoidosis, polyneuritis and chronic obstructive pulmonary disease (COPD), CNS inflammatory disorders, skin hypersensitivity disorders such as poison ivy and poison oak, B-cell malignancies such as chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host disease and cancer. The invention is also useful in gene therapy. The present sequence is human CD1a I-domain protein. This sequence is used in the exemplification of the invention.
 XX

RESULT 9
 ID ADR03370 standard; protein: 184 AA.
 XX AC ADR03370;
 XX DT 21-OCT-2004 (first entry)
 XX Human CD1a I-domain protein.
 XX CD1a antibody; human immunodeficiency virus infection; HIV infection;
 XX rhinovirus infection; inflammatory skin disease; Psoriasis;
 XX inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 XX adult respiratory distress syndrome; asthma; allergic eczema; asthma;
 XX autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;

XX Modulating binding interactions between alpha/beta proteins comprising an allosteric regulatory site, and a binding partner, by contacting with an allosteric effector molecule that interacts with the regulatory site.

Disclosure: Fig 1, 163pp; English.

XX The present sequence is the protein sequence of the integrin (1) domain of lymphocytes that associates with integrin (1) (IgA1). The invention provides methods of modulating the IgA1 domain-containing fragment of LFA-1, which is not LFA-1 or an IgA1 domain-containing fragment of LFA-1, and a binding partner. The first molecule has an alpha/beta domain, a structure comprising an allosteric regulatory site. Modulation of the binding interaction involves contacting with an allosteric effector molecule that interacts with the regulatory site. In vivo methods are also expected to alleviate and/or prevent pathological states arising from aberrant binding activity. Methods for identifying modulators are also provided.

XX Sequence 180 AA;

Query Match Score 282.5; DB 5; Length 180;
Best Local Similarity 33.5%; Pred. No. 1..3e-22;
Matches 61; Conservative 67; Mismatches 67; Gaps 2;

Qy 7 DIAFLDGSGSIIPHDRMKEPVSTMEQLKSKTFLSFLQYSSEBFRIHPTKEFONNP 66

Db 4 DLFVFLDPSMSLQDDEFQKLDFKQDMKLNLTQYPAVQFSTSYKTEPDSVYKHK 63

Qy 67 NPSILVKPTOLCRLRHTATGIRKVBLNLNTGARNPKLIVVTDGKEFDPLGYS 126

Db 64 DPDALKVKKMILMTNGANVYATEVREBLGARDATKVLILITDGS- ATDSGN1 121

Qy 127 DVIPEADREGVTVRYGVEDAPBESKSRQSLANTIAKSPDHYFQVNNEALKTIONQIR 186

Db 122 DAQKD---ITRIVIGKHTQKTESOETLHKPASKPASEFYLDFKLDFEQ 176

Qy 187 BK 188

Db 177 KK 178

RESULT 12

AYY82350 ID AYY82350 standard; protein: 184 AA.

XX AAY82350;

XX DT 22-UN-2000 (first entry)

XX DB Rhesus CD11a I-domain amino acid sequence SEQ ID NO: 8.

XX Humanized anti-CD11a antibody; anti-inflammatory; immunosuppressant;

XX antitumour; antiviral; inflammation; immunological response; LFA-1;

XX inflammatory bowel disease; associated antigen-1; psoriasis; rhinitis; eczema;

XX viral infection; transplant rejection; systemic lupus erythematosus; leukaemia;

XX Macaca mulatta.

XX PN US6037454-A.

XX 14-MAR-2000.

XX 20-NOV-1997; 97US-00574699.

XX 27-NOV-1996; 96US-0031971P.

XX (GENTECH INC.

XX Jardieu PN, Presta LG;

XX WPI; 2000-282241/24.

XX New humanized anti-CD11a antibody, useful for treating or preventing e.g. PR inflammation and transplant rejection, contains human heavy variable PR region complementarity determining regions.

XX Example: Fig 2, 38pp; English.

XX The present invention describes a humanised anti-CD11a antibody (Ab) that binds specifically to the human CD11a I-domain. The Ab has anti-inflammatory, immunosuppressive, antitumour and antiviral activities. The Ab blocks lymphocyte function-associated antigen (LFA-1), which is involved in leukocyte adhesion associated with inflammatory and immunological responses. The Ab are used: (i) optionally when coupled to a cyclocon, co-cytokine or prevent diacidoce mediated by lymphocyte function-associated antigen (CD11a/CD11b); (ii) for seborrhoea, inflammatory bowel disease, eczema, systemic lupus erythematosus, rhinitis, leukaemia, viral infections and many others; also for inhibiting graft rejection; (iii) when linked to detect CD11a; (iv) for tumour prevention; (iv) for delivery of enzymes that convert products to active anticancer agent; and (v) for affinity chromatography. The Ab retains about the same activity in adhesion and mixed lymphocyte response assays as the murine antibodies from which they are derived. The murine anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion between Jurkat cells expressing LFA-1 and normal epithelial keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).

XX The fully humanized version of MHM24 had IC50 0.13 nM. The present sequence represents the amino acid sequence of the rhesus CD11a I-domain, which is used in the exemplification of the present invention.

XX which is used in the exemplification of the present invention

SO Sequence 184 AA;

Query Match Score 29.2%; DB 3; Length 184;
Best Local Similarity 33.0%; Pred. No. 1..7e-22;
Matches 60; Conservative 48; Mismatches 67; Gaps 2;

Qy 7 DIAPUDGSSIIPHDRMKEPVSTMQLEKSTLPSLMOYSSEBFRIHPTKEFONNP 66

Db 5 DLIEFLFGNSASLQDPSDFQKLDPKDMVCKLNTSYQFAAVOFSTSYKTSDFDIDVVKOK 64

Qy 67 NPRLSVKPTOLCRLRHTATGIRKVBLNLNTGARNPKLIVVTDGKEFDPLGYS 126

Db 65 DDALIENHFMILLTNGFAGINVATYPRELGAPDPDKVLLIITDGB--ATDSGN1 122

Db 127 DVIPEADREGVTVRYGVEDAPBESKSRQSLANTIAKSPDHYFQVNNEALKTIONQIR 186

Qy 128 DIAKQD---IRVIIIGKHFQTRSSQSTLHKPASKPASEFYLDFKLDFEQ 177

Db 123 DIAKQD---IRVIIIGKHFQTRSSQSTLHKPASKPASEFYLDFKLDFEQ 177

Qy 187 BK 188

Db 178 KK 179

RESULT 13

AD538996 ID AD538996 standard; protein: 184 AA.

XX AC AD538996;

XX DT 26-FEB-2004 (first entry)

XX DB Monkey CD11a I-domain.

XX KW Monkey; CD11a; I-domain; monoclonal antibody;

XX KW cluster of differentiation 11a; mixed lymphocyte response assay;

XX KW Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;

XX KW ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;

XX KW psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;

XX KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;

XX KW diabetes mellitus; prodrg activating enzyme.

XX OS Macaca mulatta.

XX PN US2003207336-A1.

XX PD 05-NOV-2003.
 XX PP 28-FEB-2001; 2001US-00795798.
 PR 27-NOV-1996; 96US-0031971P.
 PR 20-NOV-1997; 97US-0074499.
 PR 20-OCT-1999; 99US-00420745.
 XX (GETH) GENENTECH INC.
 XX Jardieu PM, Presta LG:
 PI WPI: 2004-051511/05.
 DR XX
 XX Humanized anti-CD11a antibody useful for treating lymphocyte function-associated antigen mediated disorder e.g. psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
 Example: SEQ ID NO 8; 43pp; English.
 XX
 The invention relates to a humanised antibody cluster of differentiation (CD11a) antibody having specificity to human CD11a-domain or CD11a with a Kd value of not more than 1x10⁻⁸ M, or concentration for 50 % inhibition (IC50) value of not more than 1 nM in mixed lymphocyte response assay or for preventing adhesion of Jurkat cells to normal human epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)-1. Also included are a kit comprising the antibody and instructions for use to detect the CD11a protein, an isolated nucleic acid encoding the antibody, a vector comprising the nucleic acid, host cell comprising the vector and producing the antibody by culturing the cell so that the antibody is expressed. The antibody binds to epitope NHM24 on CD11a. The antibody is useful for determining the presence of CD11a protein and for treating lymphocyte function-associated antigen 1 mediated disorder such as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis and diabetes mellitus. The antibody is useful when conjugated to a prodring activating enzyme, or as an affinity purification agent. The present sequence is the Monkey CD11a I-domain, the target for a rheumatised antibody of the invention.
 XX Sequence 184 AA;
 Query Match Score 281.5; DB 8; Length 184;
 Best Local Similarity 11.0%; Pct. No. 1.7e-22;
 Matches 60; Conservative 48; Mismatches 67; Indels 7; Gaps 2;
 Qy 7 DTAFLDQSS1IPDPMRMEKPUSTYPMQLKSKTFLPSLMQYSSEFRINPTKEQQNNP 66
 Db 5 DLFLPDQSS1QDPDFQNLDFKMDKMKLKLNTSYOAVQTSFATKEDSDVYRQK 64
 Qy 67 NPSLSLVKEITQIQLRHTATIIRKVRLEPNITGARKNPKLIVV1D0SGKQDPLGVB 126
 Db 65 DPDALLERVHMLLNTGAIYVATEYPRLEGDPDTPVLLIDGB--ADISGRNI 122
 Qy 127 DVPFDADREGVTVYVIGDAPRSERKSROELNITASKPDPDVQVNPFALATIONOL 186
 Db 123 DIAKD----IRVIIIGKHFOTKESQSTLHKPKASBFPVKTDFKLDTPLQ 177
 Qy 187 EK 188
 Db 178 KK 179

XX KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hyperensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy; rhesus macaque.
 XX OS Macaca mulatta.
 XX Key Location/Qualifiers
 PT Region 3..11 "Beta strand 1"
 PT Region 19..34 "Alpha helix 1"
 PT Region 39..53 "Alpha helix 1"
 PT Region 57..62 "Beta strand 2"
 PT Region 67..71 "Alpha helix 2"
 PT Region 82..93 "Alpha helix 3"
 PT Region 105..112 "Alpha helix 4"
 PT Region 122..126 "Beta strand 3"
 PT Region 129..135 "Alpha helix 5"
 PT Region 142..151 "Beta strand 4"
 PT Region 160..163 "Alpha helix 6"
 PT Region 167..176 "Beta strand 5"
 PT Region 177..180 "Alpha helix 7"
 XX US2004146507-A1.
 XX PD 29-JUL-2004.
 XX PF 03-DEC-2003; 2003US-00727737.
 XX PR 27-NOV-1996; 96US-0031945P.
 XX PR 20-NOV-1997; 97US-00975329.
 XX (GETH) GENENTECH INC.
 XX Jardieu PM, Presta LG;
 XX DR WPI; 2004-552640/5A.
 XX New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 disease, allergic conditions, autoimmune diseases, or cancer.
 XX PS Example; SEQ ID NO 8; Sapp; English.
 XX CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory diseases such as
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD) , CNS inflammatory disorder, skin hyperactivity

RESULT 14
 ID ADR03371 Standard; protein: 184 AA.
 XX AC ADR03371;
 DT 21-OCT-2004 (first entry)
 DB Rhesus macaque CD11a I-domain protein.

disorders such as poison ivy and poison oak. B-cell malignancies such as chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host disease and cancer. The invention is also useful in gene therapy. The present sequence is Rhoeanus macaque CD11a I-domain protein. This sequence is used in the exemplification of the invention.

Sequence 184 AA:

```

Query Match 29.2%; Score 281.5; DB 8; Length 184;
Best Local Similarity 31.0%; Pid: No. 1.7e-22; Matches 60; Conservative 48; Mismatches 67; Indels 7; Gaps 2;
Matches 60; Conservative 48; Mismatches 67; Indels 7; Gaps 2;

Qy 7 DIAPIRDKSSGILIEHPRMKRPEVSTIMBOLKKSRTLIFSLMOMYSSEFRIHTPKEFQNNP 66
Db 5 DLIPIFQDSMQLQDQEFLQILQPKMDYKALANTSYQPAVAVQFSTSYKTFBDSDTVRK 64
Qy 67 NPSLSVKPITOLURTHATGTRKVBLPLNTGARKAFKLQVDTGKGFDPLGVB 126
Db 65 DPDALLERVKVMLLTNTGAINVTAVVERBLLEARDTAKVLLIRTDG- ATDOSGRN 122
Qy 127 DIVPSADRBGVIVRIVIGQDARRSKGRQLAINTASKEPDHYFQVNINFALKTIONQQR 186
Db 123 DAADK----IIRVIGICKHFTKESQTLIKFASKPASBVFKILDTEBKLDLTELQ 177
Qy 187 KK 188
Db 178 KK 179

```

RESULT 15
ID AAU76848 standard; protein: 184 AA.
XX
AC AAU76848;
DT 21-MAY-2002 (first entry)
XX Human integrin alpha subunit CD11a domain.
DS
Human; integrin alpha subunit; A domain; CD11a; integrin beta subunit;
KW A-like domain; inflammatory disorder; skeletal muscle injury; reticulosis;
KW ischaemia-reperfusion injury; immune complex; parasitic disease;
KW antiinflammatory; vasoconstrictor; vasoconstrictive; vasoconstrictive;
KW antiparasitic; vasoconstrictive; vasoconstrictive; vasoconstrictive; gene therapy.
OS Homo sapiens.
XX
Key Location/Qualifiers
FT 1..181 "This region is specifically claimed"
XX
PN WO200209737-A1.
XX
PD 07-FEB-2002.
XX
PP 31-JUL-2001; 2001WO-US023957.
XX
PT 31-JUL-2000; 2000US-0221950P.
PR 11-JAN-2001; 2001US-00758493.
PR 13-MAR-2001; 2001US-00005354.
XX
(GENO) GRN HOSPITAL CORP.
PA Arnaut AM, Li R, Xiong J;
XX
DR 2002-168687/24.
XX
Novel high affinity integrin polypeptide useful for treating restenosis
PT and parasitic diseases; comprises all or part of variant integrin alpha
PT subunit A domain or variant integrin beta subunit A-like domain.
PS Fig 5: 55pp; English.
XX The invention relates to a high affinity integrin polypeptide comprising
CC

all or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit, where I at residue 312 has been replaced by C, or G or A, P at residue 313 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, is useful for determining if a test compound is a candidate compound for binding to CD11b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing skeletal muscle injury, for treating disorders caused by ischaemia-reperfusion injury, immune complexes, restenosis, parasitic diseases, two-hybrid or three-hybrid assays. This sequence represents the human integrin alpha subunit CD11a domain.

Sequence 184 AA:

```

Query Match 28.7%; Score 276.5; DB 5; Length 184;
Best Local Similarity 33.0%; Pid: No. 6.6e-22; Matches 61; Indels 7; Gaps 2;
Matches 62; Conservative 48; Mismatches 71; Indels 7; Gaps 2;

Qy 1 CPOBDSIALINGSSSIPDPAKKEPVTSQMSQKSKTFLSMQYSEPRIFPTK 60
Db 1 CTKGNQDVLPFGMSNTQDPEFKLDFMDVKRQNSTSQAVFSISKTKEFDS 60
Qy 61 BFQNNPNPFRPSLVRKPTQIQLGRTHTAGIRKVKRELFTINGARKNAFLVLTVOEKG 120
Db 61 DRYKHKPQDALLKHYRMALUTNIFGAINVATEFREBLGARDPATVLLQDDB--A 118
Qy 121 DPLGYTBIDVTPADERCQVTRVIGVDAFISBISRQELNTASPPRDIVPQVNFEALKT 180
Db 119 TDSGNIDAD----IIRVIGICKHFTKESQTLIKFASKPASBVFKILDTEBKLD 173
Qy 161 IONQLERK 188
Db 174 LTFELOKK 181

```

Search completed: November 14, 2005, 17:34:35
Job time : 165 secs

A	Reference number: A64100; MUID: 86688067
A	Accession: G63107
A	Status: preliminary / nucleic acid sequence not shown; translation not shown
A	Molecule type: DNA
A	Residues: 1-181 <BUL>
A	Cross-references: UNIPROT:060375; GB:U67464; GB:L67117; NID:91590852; PIDN: AAB98050.1; C
A	Genetic map position: PGR61313-61856
A	Start codon: GTG
Query Match	7.3%; Score 70.5; DB 2; Length 181;
Best Local Similarity	22.5%; Pred. No. 66;
Matches	43; Conservative 34; Mismatches 65; Indels 49; Gaps 10;
Y	OSDIAFLIDSGSISIPIHDFRMRKKEVSTYMQSLRK----SKTFSLMQLQSEBFRIHPTF 59
b	16 DSSIKSLLSA---REPFKBNESISVNLQALEMDNDTIEI---EKNFOIILNN 67
y	60 KB---FONPNPNSRSPVPTQIOLGGHTATGKVRVLFNTGARK----WAFKIL 110
b	68 RESKQSNHIIQPKVPLNLI----KVNEESTNLNLNEENCASSIPTL 117
y	111 VVTDIGKEFKDFLAGYEVDIFPAADEGSVTRVYGVGDAFESEKSRQELNTIASKP---- 155
b	118 KETTDKLK---INNESSA-TQAEFSKAVDM----LEDNRKNUDELIEKTKLKD 166
y	166 -ROHFVQVNPF 175
b	167 LKNNLQIDNF 177
RESULT 7	
Y	PO2055
Probable phage protein YPO2055 [Imported] - <i>Yersinia pestis</i> (strain CO92)	
Species: <i>Yersinia pestis</i>	
Date: 02-Nov-2001	
Sequence_revision: 02-Nov-2001	
Accession: AF0255	
Author: B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.	
Journal: J. Gen. Microbiol.	
Title: The Yersinia pestis plague bacillus: a molecular analysis.	
Year: 1991	
Abstract: The genome sequence of <i>Yersinia pestis</i> , the causative agent of plague.	
Reference number: AB0001; MUID: 2147011; PMID: 11563630	
Accession: AF0255	
Status: preliminary	
Molecule type: DNA	
Residues: 1-187 <KUR>	
Cross-references: UNIPROT:Q8ZER2; GB:AU590842; PIDN:GAC90906.1; PIDN:9159080104; GSPPDB.C	
Genetics:	
Y	YPO2033
Query Match	7.3%; Score 70.5; DB 2; Length 187;
Best Local Similarity	25.0%; Pred. No. 69;
Matches	35; Conservative 31; Mismatches 33; Indels 53; Gaps 7;
y	43 LFSLMQSEER----THTFKFERNPNFRNPSLVKPTIQLGRTHTATGIRVVERBLNT 99
b	88 MFAPIEAKFVKWLDIKEVGNFTP----PVITPTV-----KVPNEL--- 127
y	100 NGARKNAFLVILVTOGEFGPGLQYEDVPEADREGVTVVGVDAFRSBKSRQELNT 159
b	128 ---KSRTVRVITYD-EFGRCL-----ELIGKADTR-----T 157
y	160 IASKPRDHVQVNPFALK 179

b 158 IASIGIATDGLPKPGRGVAQ 177
 RESULT 8
 H9159
 hypothetical protein MTH458 - Methanobacterium thermoautotrophicum (strain Delta H)
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #Text_change 09-Jul-204
 C:Accession: HF9159
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.
 RESULT 10
 H9159
 hypothetical protein MTH458 - Methanobacterium thermoautotrophicum (strain Delta H)
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #Text_change 09-Jul-204
 C:Accession: HF9159
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.
 b 158 IASIGIATDGLPKPGRGVAQ 177

A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-171 <KUR>
 A: Cross-references: UNIPROT:Q97N29; GB:AE001437; PID:AAK77996.1; PMID:g1502827; GSDB:Q
 A: Experimental source: Clostridium acetobutylicum ATCCB24
 C: Genetics:
 A:Gene: CAC0099

Query Match Score 6.9%; Score 67; DB 2; Length 171;
 Best Local Similarity 22.5%; Pred. No. 1.2e+0; Gaps 6;
 Matches 38; Conservative 23; Mismatches 72; Indels 36; Gaps 6;

Qy 50 SREPIINFTPKEQNPNP-----RSLVKPTITOLGRHTATGKRVREL 95
 Db 3 SBERENNIK-K-LENDDEPKKGSTLAREGYTQVTKDIALRAKGHKTAATPGCY -- 58
 Qy 96 PNTIGKARKQAFK-TLVVITDGKEKFDPDQG-----YEDVTVIBADRCGVRYVIGCD 146
 Db 59 --INNKONNSISIKRVLAVHERRAIDELNSVTKGCVNEDVIEHPLGERGILMIRT 116
 Qy 147 AFREBKSGRQEELNTISKP-----PRDHFVQDNNEFAKTNQNLREK 138
 Db 117 LFDVKNFMNKKIRDYSAEFLSILTGFQHLLTRTQNEDNNVDELTRK 165

RESULT 15

H5433
 hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans

C:Accession: H5433
 C:Date: 03-Dec-1999 Sequence_revision 03-Dec-1999 #next_change 03-Jul-2004
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, R.J.;
 S.M.; Shen, M.; Vamathevan, J.C.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 Science 26, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MNUD:20016396; PMID:10567266
 A:Accession: H5433
 A:Status: Preliminary
 A: Molecule type: DNA
 A: Residues: 1-126 <PHI>
 A: Cross-references: UNIPROT:Q9RVA8; GB:AE001962; GB:AE000513; NID:g6458855; PMID:AAF1070
 A: Experimental source: strain R1
 C: Genetics:
 A:Gene: DR121
 A:Map position: 1

Query Match Score 6.8%; Score 66; DB 2; Length 126;
 Best Local Similarity 27.0%; Pred. No. 1e-02; Gaps 6;
 Matches 34; Conservative 18; Mismatches 50; Indels 24; Gaps 6;

Qy 80 QRTTH-----ATGIRKVPELFNNTGKRNAPKLYVITYDGSKFGDPGTVIPREAD 133
 Db 6 GRHHTHEPITRASHWV-YDQVFLARQRLIVCISLV----NDRGGDLRHHSVATDD 60
 Qy 134 REGV-----RYVTVGDAF----RSBSKROBLNTIASPPRD---HVPQVNNEFAEAKT 180
 Db 61 PAQAVRHAARFYAGKGNVFSAARNARVWRAEQLTTQDLSRDTLDFTQDEFETLAA 120
 Qy 181 IONQLR 186
 Db 121 VDRLR 126

Search completed: November 14, 2005, 17:38:17
 Job time : 40 secs

Search completed: November 14, 2005, 17:37:33
Job time : 175 secs

11] RNP SEQUENCE FROM N. A.
STRAN=1C5;
MEDLINE=2012-051892; PubMed=11058132; DOI=10.1093/nar/gqz21.21.4317;
Takami H., Nakase K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Puji P., Hirama C., Nakamura Y., Ogawa S., Kubara N.,
Horikoshi K.; "Complete genome sequence of the alkylphilic bacterium *Bacillus halophilus* and genomic sequence comparison with *Bacillus subtilis*".
Nucleic Acids Res 28:4317-4331 (2000).

ENBL: AP001514; BAB05920.1; -.
 PIR: A33925; A33925.
 IntePro: IPR007353; DUF421.
 Pfam: PF04239; DUF421; 1.
 Compete proteome.
 KRW

SEQUENCE : 187 AA; 21751 MW; 33C0341D6333CS836 CRC64;

Vibrio sp. N.C.B.I.-TaxID:74109;
SEQUENCE FROM N.A.
[1] D'Angelo S., Campanaro P., Vitulo N., Lauro F.,
Cestra A., Malacrida G., Simonato B., Cannata N., Bartlett D.,
Valle G.;
"Genome analysis of Photobacterium profundum reveals the complexity of

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

ON protein - protein search, using sw model

Run on: November 14, 2005, 17:26:24 ; Search time 43 Seconds
(without alignments)

326.373 Million cell updates/sec

Title: US-09-758-493-1-COPY_1_188

Perfect score: 965

Sequence: 1 CPOBDSIAFLDGSSTIP.....VFOVNNEALKTQNQREK 188

Scoring table: BLOSUM62

Gapext 0.5

Searched: Gapext 0.5

Total number of hits satisfying chosen parameters: 387217

Minimum DB seq length: 0

Maximum DB seq length: 188

Post-processing: Minimum Match of 1
Maximum Match 100t
Listing first 45 summaries

Database :

Issued Patents M+

1: /cgn2_5/pocodata/1/iaas/SA_Comb_pep*

2: /cgn2_5/pocodata/1/iaas/SA_Comb_pep*

3: /cgn2_5/pocodata/1/iaas/6B_Comb_pep*

4: /cgn2_5/pocodata/1/iaas/PCTUS_Comb_pep*

5: /cgn2_5/pocodata/1/iaas/backfile1.pep*

6: /cgn2_5/pocodata/1/iaas/backfile1.pep*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	960	99.5	187	2	US-08-177-109A-61
2	960	99.5	187	2	US-08-687-706-61
3	534	55.3	187	2	US-08-177-109A-62
4	534	55.3	187	5	PCT-US96-01214-62
5	534	55.3	187	5	PCT-US96-01214-60
6	286.5	29.7	184	3	US-08-974-899-7
7	286.5	29.7	184	1	US-08-975-798-7
8	281.5	29.2	184	3	US-08-974-899-8
9	281.5	29.2	184	4	US-08-975-798-8
10	27.6	181	5	PCT-US96-01214-61	
11	171	17.7	33	5	PCT-US96-01214-50
12	171	17.7	33	5	PCT-US96-01214-50
13	146	15.1	28	2	US-08-476-062A-10
14	146	15.1	28	5	PCT-US96-01214-10
15	129	13.4	25	2	US-08-476-062A-8
16	129	13.4	25	5	PCT-US96-01214-8
17	126	13.1	29	5	PCT-US96-01214-68
18	125	13.0	24	5	PCT-US96-01214-69
19	117	12.1	22	2	US-08-476-062A-12
20	117	12.1	22	5	PCT-US96-01214-12
21	113	11.7	22	2	US-08-476-062A-16
22	113	11.7	22	5	PCT-US96-01214-16
23	113	11.7	22	5	PCT-US96-01214-72
24	112	11.6	21	2	US-08-476-062A-7
25	112	11.6	21	5	PCT-US96-01214-7
26	111	11.5	20	5	PCT-US96-01214-65
27	110	11.4	20	2	US-08-476-062A-17

ALIGNMENTS

RESULT 1
US-08-177-109A-61
; Sequence 61, Application US/08177109A
; Patent No. 5,869,615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oalesky
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESS: Patera L. Pabst
; STREET: 2000 One Atlantic Center
; CITY: 1201 West Peachtree Street
; STATE: Atlanta, Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release 11.1, Version #11.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/177-109A
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Patera L.
; REFERENCE/DOCKET NUMBER: 31,284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; US-08-177-109A-61

Query Match Similarity 99.5%; Score 960; DB 2; Length 187;
Best Local Similarity 100.0%; Prod. No. 3,4e-96; Mismatches 0; Indels 0; Gaps 0;
Matches 187; Conservative 0;

Qy 1 CPOBDSIAFLDGSSTIP.....VFOVNNEALKTQNQREK 60
Db 1 CPOBDSIAFLDGSSTIP.....VFOVNNEALKTQNQREK 60
Sequence 7, Appli
Sequence 7, Appli
Sequence 65, Appli
Sequence 17, Appli

*61 EFQRNPNSLVRPITQLGRHTATGIRKVRLEPLNITNGARNQAFKLVLVITDGBKFG 120

RESULT 2
 Db 61 EFGNNNRSVLUKTTQLLGRHTATGIRVRELFNTINGAKNAFKLIVTIDGEGKG 120
 Qy 121 DPLGTYDVIPEADDEGVYIYGVDPRMKEFVSTMSOLIKSKTFLSMOYSSEPRHPTFK 180
 Db 121 DPLGTYDVIPEADDEGVYIYGVDPRMKEFVSTMSOLIKSKTFLSMOYSSEPRHPTFK 180
 Qy 181 IONQLRE 187
 Db 181 IONQLRE 187

RESULT 3
 Us-08-687-706-61 Application US/08687706
 Sequence 61: Application US/08687706
 Patent No. 5928892
 General Information:
 / APPLICANT: Dennis B. Hourcade and Teresa J. Ogleby
 / TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
 / NUMBER OF SEQUENCES: 62
 / CORRESPONDENCE ADDRESS: 62
 / COMPUTER READABLE FORM:
 / ADDRESS: Patrea L. Pabst
 / STREET: 2800 One Atlantic Center
 / CITY: Atlanta
 / STATE: Georgia
 / COUNTRY: USA
 / ZIP: 30309-3450
 / COMPUTER READABLE FORM: 514
 / COMPUTER: IBM PC Compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / NUMBER: 62
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Patrea L.
 / ADDRESS: Patrea L.
 / STREET: 2800 One Atlantic Center
 / CITY: Atlanta
 / STATE: Georgia
 / COUNTRY: USA
 / ZIP: 30309-3450
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC Compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / NUMBER: 62
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Patrea L.
 / ADDRESS: Patrea L.
 / STREET: 2800 One Atlantic Center
 / CITY: Atlanta
 / STATE: Georgia
 / COUNTRY: USA
 / ZIP: 30309-3450
 / PRIORITY NUMBER: WU 107 DIV
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (404) 873-8794
 / FILING DATE: 26-JUL-1996
 / CLASIFICATION: 514
 / PRIORITY NUMBER: WU 107 DIV
 / PRIORITY NUMBER: US 08/177,109
 / FILING DATE: 03-JAN-1994
 / CLASSIFICATION: 514
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 187
 / TYPE: amino acids
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / HYPOTHETICAL: NO
 /
 Us-08-177-109A-62

Query Match 55.3%; Score 534; DB 2; Length 187;
 Best Local Similarity 55.6%; Pred. No. 5.4e-50; Indels 0; Gaps 0;
 Matches 34; Conservative 34; Mismatches 49; Delmiss 0;

Qy 1 CPQEDSDAFLIDGSGSIIPHDPRMKEFVSTMSOLIKSKTFLSMOYSSEPRHPTFK 60
 Db 1 CPQEDSDAFLIDGSGSIIPHDPRMKEFVSTMSOLIKSKTFLSMOYSSEPRHPTFK 60
 Qy 61 EFGNNNRSVLUKTTQLLGRHTATGIRVRELFNTINGAKNAFKLIVTIDGEGKG 120
 Db 61 EFGNNNRSVLUKTTQLLGRHTATGIRVRELFNTINGAKNAFKLIVTIDGEGKG 120
 Qy 121 DPLGTYDVIPEADDEGVYIYGVDPRMKEFVSTMSOLIKSKTFLSMOYSSEPRHPTFK 180
 Db 121 DPLGTYDVIPEADDEGVYIYGVDPRMKEFVSTMSOLIKSKTFLSMOYSSEPRHPTFK 180
 Qy 181 IONQLRE 187
 Db 181 IONQLRE 187

RESULT 4
 Us-08-687-706-62 Application US/08687706
 Sequence 62: Application US/08687706
 Patent No. 5928892
 General Information:
 / APPLICANT: Dennis B. Hourcade and Teresa J. Ogleby

TITLE OF INVENTION: MODIFIED COMPLEMENT PROTBASES
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS: Pabst, L., Pabst
 STREET: 2800 One Atlantic Center
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30309-3450
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/177,109
 FILING DATE: 26-JUL-1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/177,109
 FILING DATE: 03-JAN-1994
 CLASSTIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Pabst, Parrea L.
 REGISTRATION NUMBER: 31,284
 REREGISTRATION NUMBER: WU 107 DIV
 TELEPHONE: (404) 873-8794
 TELEFAX: (404) 873-8795
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCES CHARACTERISTICS:
 LENGTH: 187 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 US-08-687-706-62

Query Match Score 534; DB 2; Length 187;
 Best Local Similarity 55.6%; Prod No. 5.4e-50;
 Matches 104; Conservative 34; Mismatches 49; Indels 0; Gaps 0;

Qy 1 CPQDSIALIDGGSSTIPHDPRMKVPTMOLKKSTLSQLQSEFRHHTPK 60
 Db 1 CPQDSIALIDGGSSTIPHDPRMKVPTMOLKKSTLSQLQSEFRHHTPK 60

Qy 61 EPQNPPIPSLVKPTQLGRITAGKVRRELFTINGARNQAKLIVTGF 120
 Db 61 EPQNPPIPSLVKPTQLGRITAGKVRRELFTINGARNQAKLIVTGF 120

Qy 61 EPQNPPIPSLVKPTQLGRITAGKVRRELFTINGARNQAKLIVTGF 120
 Db 61 EPQNPPIPSLVKPTQLGRITAGKVRRELFTINGARNQAKLIVTGF 120

Qy 121 DPLGYEDVIFPDRGVTRVIGVGLAFQNRNSKELNDIAKSPSKQHFKVEDFDALKD 180
 Db 121 DPLGYEDVIFPDRGVTRVIGVGLAFQNRNSKELNDIAKSPSKQHFKVEDFDALKD 180

Qy 181 TONOLRE 187
 Db 181 TONOLRE 187

RESULT 5
 PCT-US96-01314-60
 Sequence 60, Application PC/TUS9601314
 GENERAL INFORMATION:
 APPLICANT: Amin Aranout
 TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
 TITLE OF INVENTION: ANTAGONISTS
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fieh E. Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts

RESULT 5
 PCT-US96-01314-60
 Sequence 60, Application PC/TUS9601314
 GENERAL INFORMATION:
 APPLICANT: Amin Aranout
 TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
 TITLE OF INVENTION: ANTAGONISTS
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fieh E. Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts

COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 50Z or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: Winperfect
 CURRENT APPLICATION DATA: PCT/US96/01314
 APPLICATION NUMBER: PCT/US96/01314
 FILING DATE: 30-JAN-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/180,167
 FILING DATE: 30-JAN-95
 ATTORNEY/AGENT INFORMATION:
 NAME: John W. Freeman
 REGISTRATION NUMBER: 29,066
 REFERENCE/DOCKET NUMBER: 007786/267001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEX/FAX: 200154
 INFORMATION FOR SEQ ID NO: 60:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 187 amino acids
 TYPE: amino acid
 STRANDEDNESS: Linear
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 PCT-US96-01314-60

Query Match Score 534; DB 5; Length 187;
 Best Local Similarity 55.6%; Prod. No. 5.4e-50;
 Matches 104; Conservative 34; Mismatches 49; Indels 0; Gaps 0;

Qy 1 CPQDSIALIDGGSSTIPHDPRMKVPTMOLKKSTLSQLQSEFRHHTPK 60
 Db 1 CPQDSIALIDGGSSTIPHDPRMKVPTMOLKKSTLSQLQSEFRHHTPK 60

Qy 61 EPQNPPIPSLVKPTQLGRITAGKVRRELFTINGARNQAKLIVTGF 120
 Db 61 EPQNPPIPSLVKPTQLGRITAGKVRRELFTINGARNQAKLIVTGF 120

Qy 121 DPLGYEDVIFPDRGVTRVIGVGLAFQNRNSKELNDIAKSPSKQHFKVEDFDALKD 180
 Db 121 DPLGYEDVIFPDRGVTRVIGVGLAFQNRNSKELNDIAKSPSKQHFKVEDFDALKD 180

Qy 181 TONOLRE 187
 Db 181 TONOLRE 187

RESULT 6
 US-08-774-899-7 Application US/08974899
 GENERAL INFORMATION:
 APPLICANT: Presta, Leonard M.
 APPLICANT: Jardieu, Paula M.
 TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 PATENT NO. 603754
 ADDRESS: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPcap (Genentech)
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974, 899
 FILING DATE: 11/27/96
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/031971
 FILING DATE: 11/27/96
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P1014R1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/952-9881
 TELEFAX: 650/952-9881
 SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-974-899-7

Query Match 29.7%; Score 286.5; DB 3; Length 184;
 Best Local Similarity 33.3%; Pred. No. 3.6e-23; Gaps 2;
 Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;

Qy 7 DIAPIUDGSGSIIPHDPRMKVFSKTKLPSMQLIKSKRTIPLSMOYSBEPRIHPTKEFQNNP 66
 Db 5 DIAPIUDGSGSIIPHDPRMKVFSKTKLPSMQLIKSKRTIPLSMOYSBEPRIHPTKEFQNNP 66
 Qy 67 NPIRSVKEKTTOLIGRHTATGIRKVRLBFLNTGARKNPKFLVYTDGEKGDFGLYB 126
 Db 65 DPDALLKHVKHMLLNFGAINVNTTATGKPLDVKLVLITDE--ATSGNI 122
 Qy 127 DVIPEADREGVIVYVGDAFPRSERKSERELNTASKPPDVIYGVNNFALKTIONQL 186
 Db 123 DIAKD---IIRYIGRHPQTKEQSTLHKFASPVKLDPEKLDFLTBLQ 177
 Qy 187 EK 188
 Db 178 KK 179

RESULT 7
 Sequence 7, Application US/09/795798
 Patent No. 67031018
 GENERAL INFORMATION:
 APPLICANT: Preata, Leonard G.
 ATTORNEY/AGENT INFORMATION:
 Jardieu, Paula M.
 TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/795, 798
 FILING DATE: 28-Feb-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/974, 899
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P1014R1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/925-1994
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-795,798-7

Query Match 29.7%; Score 286.5; DB 4; Length 184;
 Best Local Similarity 33.5%; Pred. No. 3.6e-23; Gaps 2;
 Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;

Qy 7 DIAPIUDGSGSIIPHDPRMKVFSKTKLPSMQLIKSKRTIPLSMOYSBEPRIHPTKEFQNNP 66
 Db 5 DIAPIUDGSGSIIPHDPRMKVFSKTKLPSMQLIKSKRTIPLSMOYSBEPRIHPTKEFQNNP 66
 Qy 67 NPIRLVKPITQDQGLRTATGARKNPKFLVYTDGEKGDFGLYB 126
 Db 65 DEDALLKHVKHMLLNFGAINVNTTATGKPLDVKLVLITDE--ATSGNI 122
 Qy 127 DVIPEADREGVIVYVGDAFPRSERKSERELNTASKPPDVIYGVNNFALKTIONQL 186
 Db 123 DIAKD---IIRYIGRHPQTKEQSTLHKFASPVKLDPEKLDFLTBLQ 177
 Qy 187 EK 188
 Db 178 KK 179

RESULT 8
 Sequence 8, Application US/08/974899
 Patent No. 6037454
 GENERAL INFORMATION:
 APPLICANT: Preata, Leonard G.
 ATTORNEY/AGENT INFORMATION:
 Jardieu, Paula M.
 TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974, 899
 FILING DATE:
 CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/031971
 FILING DATE: 11/27/96
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P1014R1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/925-1994
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 184 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-974-899-8

Query Match	Score 29.2%; Best Local Similarity 33.0%; Matches 60; Conservative 48;	Score 281.5%; Pred. No. 1.3e-22; Mismatches 67; Indexes 2;	Length 184;
Query	7 DIAFLDGSSTIIPDFRANKRKFVSTMEOLKSKTSLMSWYSBFRHTPFBFNNNP 56 5 DULPFDGMSLQDPEKIDMVKMKTLSNTSYOAAVQESTSYKTEDSYKQ 64	67 NPSLVLKVITDPLGRTHTATGIRKVRBELNTIAGRNAPKLVWITDGEKEFCDFLGW 126 65 DPDALIENKVEMLLINTGCAVNTVANEVREPLGFARPKVLTTCG -ATDSGN1 122	127 DVPIADERGIVRYKIVGCDATRSERKSPRINTISKEPRDRYFONNFEALKTIONQLR 186 123 DAAD --- IRYVIGKHPKTESQETLKFAKSPASEFVKILDPEKLUODLPBQ 177
Db	Db	Db	Db
Query	187 BK 188	178 KK 179	187 BK 188
Db	Db	Db	Db
RESULT 9			
US-09-795-198-B			
Sequence 8, Application US/09795798	Pred. No. 6703018	Length 184;	Length 177
Patent	GENERAL INFORMATION:	SEQUENCE DESCRIPTION:	SEQUENCE DESCRIPTION:
APPLICANT: Prentiss, Leonard G.	APPLICANT: Jardine, Paula M.	APPLICANT: Leonard G.	APPLICANT: Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies	NUMBER OF SEQUENCES: 24	TITLE OF INVENTION: Humanized Anti-CD11a Antibodies	TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
CORRESPONDENCE ADDRESS:	ADDRESS: Genentech, Inc.	CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.	STREET: 1 DNA Way	ADDRESS: Genentech, Inc.	ADDRESS: Genentech, Inc.
CITY: South San Francisco	CITY: South San Francisco	CITY: South San Francisco	CITY: South San Francisco
STATE: California	STATE: California	STATE: California	STATE: California
COUNTRY: USA	COUNTRY: USA	COUNTRY: USA	COUNTRY: USA
ZIP: 94090	ZIP: 94090	ZIP: 94090	ZIP: 94090
COMPUTER READABLE FORM:	COMPUTER READABLE FORM:	COMPUTER READABLE FORM:	COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk	MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk	MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk	MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS	OPERATING SYSTEM: PC-DOS/NS-DOS	OPERATING SYSTEM: PC-DOS/NS-DOS	OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: WinPatin (Genentech)	SOFTWARE: WinPatin (Genentech)	SOFTWARE: WinPatin (Genentech)	SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/09/795-798	CURRENT APPLICATION NUMBER: US/09/795-798	CURRENT APPLICATION NUMBER: US/09/795-798	CURRENT APPLICATION NUMBER: US/09/795-798
FILING DATE: 28-Feb-2001	FILING DATE: 28-Feb-2001	FILING DATE: 28-Feb-2001	FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>	CLASSIFICATION: <Unknown>	CLASSIFICATION: <Unknown>	CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974, 899	APPLICATION NUMBER: 08/974, 899	APPLICATION NUMBER: 08/974, 899	APPLICATION NUMBER: 08/974, 899
FILING DATE: <Unknown>	FILING DATE: <Unknown>	FILING DATE: <Unknown>	FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.	NAME: Lee, Wendy M.	NAME: Lee, Wendy M.	NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378	REGISTRATION NUMBER: 40,378	REGISTRATION NUMBER: 40,378	REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014RL	REFERENCE/DOCKET NUMBER: P1014RL	REFERENCE/DOCKET NUMBER: P1014RL	REFERENCE/DOCKET NUMBER: P1014RL
TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1394	TELEPHONE: 650/225-1394	TELEPHONE: 650/225-1394	TELEPHONE: 650/225-1394
TELEFAX: 650/952-9881	TELEFAX: 650/952-9881	TELEFAX: 650/952-9881	TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:	INFORMATION FOR SEQ ID NO: 8:	INFORMATION FOR SEQ ID NO: 8:	INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids	LENGTH: 184 amino acids	LENGTH: 184 amino acids	LENGTH: 184 amino acids
TYPE: protein	TYPE: protein	TYPE: protein	TYPE: protein
TOPOLOGY: linear	TOPOLOGY: linear	TOPOLOGY: linear	TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:	SEQUENCE DESCRIPTION: SEQ ID NO: 8:	SEQUENCE DESCRIPTION: SEQ ID NO: 8:	SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-795-198-B	US-09-795-198-B	US-09-795-198-B	US-09-795-198-B
Query Match	Score 29.2%; Best Local Similarity 33.0%; Matches 60; Conservative 48;	Score 281.5%; Pred. No. 1.3e-22; Mismatches 67; Indexes 7;	Score 281.5%; Pred. No. 1.3e-22; Mismatches 67; Indexes 7;
Query	7 DIAFLDGSSTIIPDFRANKRKFVSTMEOLKSKTSLMSWYSBFRHTPFBFNNNP 56 5 DULPFDGMSLQDPEKIDMVKMKTLSNTSYOAAVQESTSYKTEDSYKQ 64	67 NPSLVLKVITDPLGRTHTATGIRKVRBELNTIAGRNAPKLVWITDGEKEFCDFLGW 126 65 DPDALIENKVEMLLINTGCAVNTVANEVREPLGFARPKVLTTCG -ATDSGN1 122	127 DVPIADERGIVRYKIVGCDATRSERKSPRINTISKEPRDRYFONNFEALKTIONQLR 186 123 DAAD --- IRYVIGKHPKTESQETLKFAKSPASEFVKILDPEKLUODLPBQ 177
Db	Db	Db	Db
RESULT 10			
PCT-US96-01114-61			
Sequence 61, Application PCT-US9601114	GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:
APPLICANT: M. Ann Arnaut	TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN	TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN	TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
STATE: Massachusetts	NUMBER OF SEQUENCES: 78	NUMBER OF SEQUENCES: 78	NUMBER OF SEQUENCES: 78
CITY: Boston	CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:
STREET: 225 Franklin Street	STREET: Fish & Richardson P.C.	STREET: Fish & Richardson P.C.	STREET: Fish & Richardson P.C.
ZIP: 02110-2804	ZIP: 02110-2804	ZIP: 02110-2804	ZIP: 02110-2804
COMPUTER READABLE FORM:	COMPUTER READABLE FORM:	COMPUTER READABLE FORM:	COMPUTER READABLE FORM:
COMPUTER: IBM PS/2 Model 502 or 55SX	COMPUTER: IBM PS/2 Model 502 or 55SX	COMPUTER: IBM PS/2 Model 502 or 55SX	COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)	OPERATING SYSTEM: MS-DOS (Version 5.0)	OPERATING SYSTEM: MS-DOS (Version 5.0)	OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)	SOFTWARE: WordPerfect (Version 5.1)	SOFTWARE: WordPerfect (Version 5.1)	SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT-US96/01114	APPLICATION NUMBER: PCT-US96/01114	APPLICATION NUMBER: PCT-US96/01114	APPLICATION NUMBER: PCT-US96/01114
FILING DATE: 30-JAN-96	FILING DATE: 30-JAN-96	FILING DATE: 30-JAN-96	FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380, 67	APPLICATION NUMBER: 08/380, 67	APPLICATION NUMBER: 08/380, 67	APPLICATION NUMBER: 08/380, 67
FILING DATE: 30-JAN-95	FILING DATE: 30-JAN-95	FILING DATE: 30-JAN-95	FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman	NAME: John W. Freeman	NAME: John W. Freeman	NAME: John W. Freeman
REGISTRATION NUMBER: 29,066	REGISTRATION NUMBER: 29,066	REGISTRATION NUMBER: 29,066	REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/267001	REFERENCE/DOCKET NUMBER: 00786/267001	REFERENCE/DOCKET NUMBER: 00786/267001	REFERENCE/DOCKET NUMBER: 00786/267001
TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-9570	TELEPHONE: (617) 542-9570	TELEPHONE: (617) 542-9570	TELEPHONE: (617) 542-9570
TELEFAX: (617) 542-9906	TELEFAX: (617) 542-9906	TELEFAX: (617) 542-9906	TELEFAX: (617) 542-9906
TELEX: 200154	TELEX: 200154	TELEX: 200154	TELEX: 200154
INFORMATION FOR SEQ ID NO: 61:	INFORMATION FOR SEQ ID NO: 61:	INFORMATION FOR SEQ ID NO: 61:	INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids	LENGTH: 181 amino acids	LENGTH: 181 amino acids	LENGTH: 181 amino acids
TYPE: amino acid	TYPE: amino acid	TYPE: amino acid	TYPE: amino acid
SPRANDSBORGSS:	SPRANDSBORGSS:	SPRANDSBORGSS:	SPRANDSBORGSS:
TOPOLOGY: linear	TOPOLOGY: linear	TOPOLOGY: linear	TOPOLOGY: linear
MOLECULE TYPE: protein	MOLECULE TYPE: protein	MOLECULE TYPE: protein	MOLECULE TYPE: protein
PCT-US96-01114-61	PCT-US96-01114-61	PCT-US96-01114-61	PCT-US96-01114-61
Query Match	Score 27.6%; Best Local Similarity 31.0%; Matches 60; Conservative 46;	Score 27.6%; Best Local Similarity 31.0%; Matches 60; Conservative 46;	Score 27.6%; Best Local Similarity 31.0%; Matches 60; Conservative 46;
Query	61 BPPNNPENPLVPTIOLGRHTATGIRKVRBELNTIAGRNAPKLVWITDGEKEFCDFLGW 120 61 DYYTKMDPDALKHMLINTGCAVNTVANEVREPLGFARPKVLTTCG -ATDSGN1 118	61 BPPNNPENPLVPTIOLGRHTATGIRKVRBELNTIAGRNAPKLVWITDGEKEFCDFLGW 120 61 DYYTKMDPDALKHMLINTGCAVNTVANEVREPLGFARPKVLTTCG -ATDSGN1 118	61 BPPNNPENPLVPTIOLGRHTATGIRKVRBELNTIAGRNAPKLVWITDGEKEFCDFLGW 120 61 DYYTKMDPDALKHMLINTGCAVNTVANEVREPLGFARPKVLTTCG -ATDSGN1 118
Db	Db	Db	Db
RESULT 11			
PCT-US96-01114-61			
Sequence 61, Application PCT-US9601114	GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:
APPLICANT: M. Ann Arnaut	TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN	TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN	TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
STATE: Massachusetts	NUMBER OF SEQUENCES: 78	NUMBER OF SEQUENCES: 78	NUMBER OF SEQUENCES: 78
CITY: Boston	CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:
STREET: 225 Franklin Street	STREET: Fish & Richardson P.C.	STREET: Fish & Richardson P.C.	STREET: Fish & Richardson P.C.
ZIP: 02110-2804	ZIP: 02110-2804	ZIP: 02110-2804	ZIP: 02110-2804
COMPUTER READABLE FORM:	COMPUTER READABLE FORM:	COMPUTER READABLE FORM:	COMPUTER READABLE FORM:
COMPUTER: IBM PS/2 Model 502 or 55SX	COMPUTER: IBM PS/2 Model 502 or 55SX	COMPUTER: IBM PS/2 Model 502 or 55SX	COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)	OPERATING SYSTEM: MS-DOS (Version 5.0)	OPERATING SYSTEM: MS-DOS (Version 5.0)	OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)	SOFTWARE: WordPerfect (Version 5.1)	SOFTWARE: WordPerfect (Version 5.1)	SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT-US96/01114	APPLICATION NUMBER: PCT-US96/01114	APPLICATION NUMBER: PCT-US96/01114	APPLICATION NUMBER: PCT-US96/01114
FILING DATE: 30-JAN-96	FILING DATE: 30-JAN-96	FILING DATE: 30-JAN-96	FILING DATE: 30-JAN-96
ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman	NAME: John W. Freeman	NAME: John W. Freeman	NAME: John W. Freeman
REGISTRATION NUMBER: 29,066	REGISTRATION NUMBER: 29,066	REGISTRATION NUMBER: 29,066	REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/267001	REFERENCE/DOCKET NUMBER: 00786/267001	REFERENCE/DOCKET NUMBER: 00786/267001	REFERENCE/DOCKET NUMBER: 00786/267001
TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-9570	TELEPHONE: (617) 542-9570	TELEPHONE: (617) 542-9570	TELEPHONE: (617) 542-9570
TELEFAX: (617) 542-9906	TELEFAX: (617) 542-9906	TELEFAX: (617) 542-9906	TELEFAX: (617) 542-9906
TELEX: 200154	TELEX: 200154	TELEX: 200154	TELEX: 200154
INFORMATION FOR SEQ ID NO: 61:	INFORMATION FOR SEQ ID NO: 61:	INFORMATION FOR SEQ ID NO: 61:	INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids	LENGTH: 181 amino acids	LENGTH: 181 amino acids	LENGTH: 181 amino acids
TYPE: amino acid	TYPE: amino acid	TYPE: amino acid	TYPE: amino acid
SPRANDSBORGSS:	SPRANDSBORGSS:	SPRANDSBORGSS:	SPRANDSBORGSS:
TOPOLOGY: linear	TOPOLOGY: linear	TOPOLOGY: linear	TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 61:	SEQUENCE DESCRIPTION: SEQ ID NO: 61:	SEQUENCE DESCRIPTION: SEQ ID NO: 61:	SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-09-795-198-B	US-09-795-198-B	US-09-795-198-B	US-09-795-198-B
Query Match	Score 29.2%; Best Local Similarity 33.0%; Matches 60; Conservative 48;	Score 281.5%; Pred. No. 1.3e-22; Mismatches 67; Indexes 7;	Score 281.5%; Pred. No. 1.3e-22; Mismatches 67; Indexes 7;
Query	7 DIAFLDGSSTIIPDFRANKRKFVSTMEOLKSKTSLMSWYSBFRHTPFBFNNNP 56 5 DULPFDGMSLQDPEKIDMVKMKTLSNTSYOAAVQESTSYKTEDSYKQ 64	67 NPSLVLKVITDPLGRTHTATGIRKVRBELNTIAGRNAPKLVWITDGEKEFCDFLGW 126 65 DPDALIENKVEMLLINTGCAVNTVANEVREPLGFARPKVLTTCG -ATDSGN1 122	127 DVPIADERGIVRYKIVGCDATRSERKSPRINTISKEPRDRYFONNFEALKTIONQLR 186 123 DAAD --- IRYVIGKHPKTESQETLKFAKSPASEFVKILDPEKLUODLPBQ 177
Db	Db	Db	Db

Db 174 DL 175

RESULT 11
Sequence 50, Application US/08/476-062A-50
Patent No. 5,938,755

GENERAL INFORMATION:
APPLICANT: Arnaout, M. Anan
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY RESPONSES WITH BETA2 INTEGRINS
NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:
ADDRESS/B: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq For Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476, 062A
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/216, 081
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: 07/637, 830
FILING DATE: 04-JAN-1991
APPLICATION NUMBER: 07/539, 842
FILING DATE: 16-JUN-1990
APPLICATION NUMBER: 07/12, 573
FILING DATE: 28-JUN-1988
PRIORITY APPLICATION DATA:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29, 066
REFERENCE/DOCKET NUMBER: 00786/068003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8070
TELEFAX: 617/542-8906

TELEX: 200154

SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Peptide

US/08/476-062A-50

Query Match Score 171; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-11; Indels 0; Gaps 0;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 NAFKILVIVTDGKFGDPGLYEDVTPAAREGV 137

Db 1 NAFKILVIVTDGKFGDPGLYEDVTPAAREGV 33

RESULT 13
US/08/476-062A-10

Sequence 10, Application US/08476062A

GENERAL INFORMATION:
Patent No.: 5,877,215

APPLICANT: Arnaout, M. Anan
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY RESPONSES WITH BETA2 INTEGRINS
NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:
ADDRESSEES: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA

Query Match Score 171; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-11; Indels 0; Mismatches 0; Gaps 0;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 NAFKILVIVTDGKFGDPGLYEDVTPAAREGV 137

Db 1 NAFKILVIVTDGKFGDPGLYEDVTPAAREGV 33

RESULT 14
PCT-US/08/476-062A-50

Sequence 50, Application PC/US/08/476, 062A

GENERAL INFORMATION:
APPLICANT: M. Anan Arnaout
TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS
NUMBER OF SEQUENCES: 78

CORRESPONDENCE ADDRESS:
ADDRESSEES: Fish & Richardson P.C.
STREET: 225 Franklin Street

ATTORNEY/AGENT INFORMATION:
 NAMES: Freeman, John W.
 REGISTRATION NUMBER: 29,066
 REFERENCE/DOCKET NUMBER: 00786/088003
 TELECOMMUNICATION INFORMATION:
 TELEPAK: 617/542-8906
 TELFAX: 617/542-89070
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: Peptide
 US-08-476-062A-10

Query Match Similarity 15.1%; Score 146; DB 2; Length 28;
 Best Local Similarity 10.0%; Pred. No. 5.1e-09; Mismatches 0; Indels 0; Gaps 0;

Qy 107 PKILVVITDGEKGDKPLGYEVIPEAR 134
 Db 1 PKILVVITDGEKGDKPLGYEVIPEAR 28

RESULT 14
 PCT-US96-01314-10

SEQUENCE 10: Application PC/TUS9601314
 GENERAL INFORMATION:
 APPLICANT: M. Arnaout
 TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
 NUMBER OF SEQUENCES: 78
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette
 COMPUTER: IBM PS/2 Model 502 or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 95CT/US96/01314
 FILING DATE: 30-JAN-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 98/380,167
 FILING DATE: 20-JAN-95

ATTORNEY/AGENT INFORMATION:
 NAME: "John W. Freeman"
 REGISTRATION NUMBER: 29,066
 REFERENCE/DOCKET NUMBER: 00786/267001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-8906
 TELFAX: (617) 542-89070
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 10:
 LENGTH: 28
 TYPE: amino acid
 STRANDBNESS:
 TOPOLOGY: linear

PCT-US96-01314-10

Query Match Similarity 15.1%; Score 146; DB 5; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.1e-09; Mismatches 0; Indels 0; Gaps 0;

Qy 107 PKILVVITDGEKGDKPLGYEVIPEAR 134

SEARCH COMPLETED: November 14, 2005, 17:39:04
 Job time : 44 secs

RESULT 15
 US-08-476-062A-8

SEQUENCE 8: Application US/08476062A
 GENERAL INFORMATION:
 APPLICANT: Arnaout, M. Amin
 TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY RESPONSES WITH BETA2 INTEGRINS
 NUMBER OF INVENTIONS: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTY: US
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/476,062A
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/216,081
 FILING DATE: 21-MAR-1994

APPLICATION NUMBER: 07/637,830
 FILING DATE: 04-JAN-1991

APPLICATION NUMBER: 07/539,842
 FILING DATE: 18-JUN-1990

APPLICATION NUMBER: 07/212,573
 FILING DATE: 28-JUN-1988

ATTORNEY/AGENT INFORMATION:
 NAME: Freeman, John W.
 REGISTRATION NUMBER: 29,066
 REFERENCES/DOCKET NUMBER: 00786/068003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEX: 617/542-8906
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 amino acids
 TYPE: amino acid
 TOPOLOGY: linear peptide

US-08-476-062A-8

Query Match Similarity 13.4%; Score 129; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07; Mismatches 0; Indels 0; Gaps 0;

Qy 66 PNPRSLVKEITDOLGRHTATGIRK 90
 Db 1 PNPRSLVKEITDOLGRHTATGIRK 25

SEARCH COMPLETED: November 14, 2005, 17:39:04
 Job time : 44 secs

Result	No.	Score	Match	Length	DB	ID	Description
1	939	97.3	184	15	US-10-346-363-37		Sequence 17, Appli
2	939	97.3	187	15	US-10-346-363-37		Sequence 17, Appli
3	939	97.3	187	16	US-10-615-515-9		Sequence 9, Appli
4	514	55.3	187	20	US-11-000-173-59		Sequence 59, Appli
5	333	34.6	176	10	US-09-767-782-38		Sequence 38, Appli
6	286	29.7	182	15	US-10-346-863-33		Sequence 33, Appli
7	286	29.7	183	15	US-10-346-863-20		Sequence 20, Appli
8	286	29.7	183	15	US-10-346-863-41		Sequence 4, Appli
9	286	29.7	183	16	US-10-615-515-7		Sequence 7, Appli
10	286	29.7	184	10	US-09-895-554-4		Sequence 4, Appli
11	286	29.7	184	10	US-09-795-798-7		Sequence 7, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query	Length	DB	ID	Description
Sequence 4, Appli	11	US-09-758-493-4		
Sequence 4, Appli	14	US-10-144-259-4		
Sequence 2013, Ap	16	US-10-471-177-2033		
Sequence 7, Appli	18	US-10-727-737-7		
Sequence 35, Appli	18	US-10-346-863-36		
Sequence 36, Appli	18	US-10-346-863-56		
Sequence 56, Appli	18	US-10-699-0154-28		
Sequence 8, Appli	18	US-09-795-798-8		
Sequence 8, Appli	18	US-10-722-737-8		
Sequence 60, Appli	20	US-11-000-413-60		
Sequence 40, Appli	20	US-11-000-413-60		
Sequence 4, Appli	21	US-09-801-736A-4		
Sequence 26, Appli	21	US-10-699-0154-26		
Sequence 79, Appli	21	US-10-000-198A-79		
Sequence 28, Appli	21	US-10-346-863-43		
Sequence 41, Appli	21	US-10-346-863-31		
Sequence 31, Appli	21	US-11-007-298-3		
Sequence 31, Appli	21	US-10-080-114-30		
Sequence 12, Appli	21	US-10-699-0154-24		
Sequence 24, Appli	21	US-10-000-318A-01		
Sequence 91, Appli	21	US-10-346-863-30		
Sequence 30, Appli	21	US-10-699-0154-23		
Sequence 22, Appli	21	US-10-699-0154-22		
Sequence 23, Appli	21	US-10-699-0154-23		
Sequence 50, Appli	21	US-11-000-413-50		
Sequence 1209, Ap	21	US-10-087-192-1209		
Sequence 27, Appli	21	US-10-699-0154-27		
Sequence 29, Appli	21	US-10-699-0154-27		
Sequence 8, Appli	21	US-10-699-0154-8		
Sequence 31, Appli	21	US-10-699-0154-31		
Sequence 2, Appli	21	US-10-699-0154-2		
Sequence 3, Appli	21	US-09-801-736A-3		
Sequence 3310, A	21	US-09-864-761-3310		
Sequence 47637, A	21	US-09-864-761-47637		

ALIGNMENTS

RESULT 1
US-10-346-863-17
Sequence 17, Application US-103468633
; Publication No.: US-20040382541
; General Information:
; Applicant: CHRISTOPHER BENJAMIN
; Applicant: PAGAN, RICHARD JOSEPH
; Applicant: CUTTERIDGE, ALEX
; Title of Invention: ADHESION MOLECULES
; File Reference: 674575-2001
; Current Application Number: US-10/346,863
; Current Filing Date: 2003-01-17
; Prior Application Number: PCT/GB01/03318
; Prior Filing Date: 2001-07-24
; Prior Application Number: GB 0018126-3
; Prior Filing Date: 2000-07-24
; Prior Application Number: GB 0025447-4
; Prior Filing Date: 2000-10-17
; Number of SEQ ID NOS: 57
; Software: PatentIn Ver. 2.1
; SEQ ID: 17
; Length: 184
; Type: PRT
; Organism: Homo sapiens
US-10-346-863-17

Query Match Similarity 97.3%; Score 919; DB 15; Length 184;
Best Local Similarity 100.0%; Pred No. 7; 1e-92;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 DSDAFLIDSSIIIPDFRMMEYRSTWQKCKSYTFSLSMQYSSEPRHTKEFQN 64
Db 1 DSDAFLIDSSIIIPDFRMMEYRSTWQKCKSYTFSLSMQYSSEPRHTKEFQN 60

Qy 65 NNPRLSLVYKPTIOLGLRTHTATGIRKVYRELNTINGARNAKFLVVTIDGSKFGDPLG 124
 Db 61 NNPRLSLVYKPTIOLGLRTHTATGIRKVYRELNTINGARNAKFLVVTIDGSKFGDPLG 120
 Qy 125 YEDVIPADREGVITYVIGODAFRSKERSQLANTIASPKPRDHYFQVNNEALKTQ 184
 Db 121 YEDVIPADREGVITYVIGODAFRSKERSQLANTIASPKPRDHYFQVNNEALKTQ 180
 Qy 185 LREK 188
 Db 181 LREK 184

RESULT 2

US-10-346-663-37
 Sequence 37, Application US/10346663
 Publication No. US20040038435A1
 GENERAL INFORMATION:
 APPLICANT: PHILIPS, CHRISTOPHER BENJAMIN
 APPLICANT: FAGAN, RICHARD JOSEPH
 APPLICANT: GUTTERIDGE, ALEX
 TITLE OF INVENTION: ADHESION MOLECULES
 FILE REFERENCE: 674575-201
 CURRENT APPLICATION NUMBER: US/10/346,863
 CURRENT FILING DATE: 2003-01-17
 PRIOR APPLICATION NUMBER: PCT/GB01/03318
 PRIOR FILING DATE: 2001-07-24
 PRIOR APPLICATION NUMBER: GB 0018126,3
 PRIOR FILING DATE: 2000-07-24
 PRIOR APPLICATION NUMBER: GB 0025447,4
 PRIOR FILING DATE: 2000-01-17
 NUMBER OF SEQ ID NOS: 57
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 37
 LENGTH: 187
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-346-663-37

Query Match 97.3%; Score 939; DB 15; Length 187;
 Best Local Similarity 100.0%; Pred. No. 7.5e-32;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DSDIALPDISSGSI1PHDRMKPYSTMBLKSKTLPSLMOSEPFRIHTPEKFON 64
 Db 1 DSDIALPDISSGSI1PHDRMKPYSTMBLKSKTLPSLMOSEPFRIHTPEKFON 60
 Qy 65 NNPRLSLVYKPTIOLGLRTHTATGIRKVYRELNTINGARNAKFLVVTIDGSKFGDPLG 124
 Db 61 NNPRLSLVYKPTIOLGLRTHTATGIRKVYRELNTINGARNAKFLVVTIDGSKFGDPLG 120
 Qy 125 YEDVIPADREGVITYVIGODAFRSKERSQLANTIASPKPRDHYFQVNNEALKTQ 184
 Db 121 YEDVIPADREGVITYVIGODAFRSKERSQLANTIASPKPRDHYFQVNNEALKTQ 180
 Qy 185 LREK 188
 Db 181 LREK 184

RESULT 3

US-10-615-515-9

Sequence 9, Application US/10615515
 Publication No. US2004012974A1
 GENERAL INFORMATION:
 APPLICANT: FAGAN, RICHARD, JOSEPH
 APPLICANT: FAGAN, RICHARD, JOSEPH BENJAMIN
 APPLICANT: GUTTERIDGE, ALEX
 TITLE OF INVENTION: ADHESION MOLECULES
 FILE REFERENCE: 674575-204
 CURRENT APPLICATION NUMBER: US/10/615,515
 CURRENT FILING DATE: 2003-07-08
 PRIOR APPLICATION NUMBER: PCT/GB02/00107

Query Match 97.3%; Score 939; DB 16; Length 187;

Best Local Similarity 100.0%; Pred. No. 7.5e-32;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DSDIALPDISSGSI1PHDRMKPYSTMBLKSKTLPSLMOSEPFRIHTPEKFON 64
 Db 1 DSDIALPDISSGSI1PHDRMKPYSTMBLKSKTLPSLMOSEPFRIHTPEKFON 60
 Qy 65 NNPRLSLVYKPTIOLGLRTHTATGIRKVYRELNTINGARNAKFLVVTIDGSKFGDPLG 124
 Db 61 NNPRLSLVYKPTIOLGLRTHTATGIRKVYRELNTINGARNAKFLVVTIDGSKFGDPLG 120
 Qy 125 YEDVIPADREGVITYVIGODAFRSKERSQLANTIASPKPRDHYFQVNNEALKTQ 184
 Db 121 YEDVIPADREGVITYVIGODAFRSKERSQLANTIASPKPRDHYFQVNNEALKTQ 180
 Qy 185 LREK 188
 Db 181 LREK 184

RESULT 4

US-11-000-473-59

Sequence 59, Application US/11000473
 Publication No. US2004022796A1
 GENERAL INFORMATION:
 APPLICANT: Arnout, M. Armin
 TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS
 FILE REFERENCE: 00786-267002
 CURRENT APPLICATION NUMBER: US/11/000,473
 CURRENT FILING DATE: 2004-11-30
 PRIOR APPLICATION NUMBER: US/09/532,617
 PRIOR FILING DATE: 2000-06-13
 PRIOR APPLICATION NUMBER: US/08/390,167
 PRIOR FILING DATE: 1999-01-20
 PRIOR APPLICATION NUMBER: US/08/216,081
 PRIOR FILING DATE: 1994-03-21
 PRIOR APPLICATION NUMBER: US/07/637,830
 PRIOR FILING DATE: 1991-01-04
 PRIOR APPLICATION NUMBER: US/07/539,642
 PRIOR FILING DATE: 1990-06-18
 PRIOR APPLICATION NUMBER: US/07/212,573
 PRIOR FILING DATE: 1988-06-28
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 59
 LENGTH: 187
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-000-473-59

Query Match 55.3%; Score 534; DB 20; Length 187;

Best Local Similarity 55.6%; Pred. No. 1.5e-48;
 Matches 104; Conservative 34; Mismatches 49; Indels 0; Gaps 0;

Qy 1 CPOEDSIATLGDGGSI1PHDRMKPYSTMBLKSKTLPSLMOSEPFRIHTPEKFON 60
 Db 1 CPOEDSIATLGDGGSI1PHDRMKPYSTMBLKSKTLPSLMOSEPFRIHTPEKFON 60
 Qy 61 EPNQNPPLRPLVPLGCGISSNEMAFATMVKVRLPENITGARKNAPKILVVTIDGSKFG 120
 Db 61 EPNQNPPLRPLVPLGCGISSNEMAFATMVKVRLPENITGARKNAPKILVVTIDGSKFG 120
 Db 61 EPNQNPPLRPLVPLGCGISSNEMAFATMVKVRLPENITGARKNAPKILVVTIDGSKFG 120

Qy 121 DPLGKEDVPEADRGVTVYIGDARSKRSRQLNTIASPPRDHVFOVNNEALKT 180
Db 121 DSIDVKDPMADAGIIRYATGVLAQNRMNSKELNDASKPSQEHIKFVDEDALKD 180
Qy 181 IONOLRE 187
Db 181 IONOLKE 187

RESULT 5
US-09-976-782-38 Application US/03976782
; Sequence 38, Application US/03976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Gross et al.
; TITLE OF INVENTION: No. US20030190715A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-157
; CURRENT APPLICATION NUMBER: US/09/976, 782
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/244, 113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240, 652
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240, 732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240, 635
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240, 703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241, 190
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240, 637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240, 669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/242, 455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240, 648
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 38
; LENGTH: 176
; TYPE: PPT
; ORGANISM: Artificial Sequence
; PRATURE:
; OTHER INFORMATION: Description of Artificial Sequence : Consensus
; OTHER INFORMATION: sequence

Qy 121 DPLGKEDVPEADRGVTVYIGDARSKRSRQLNTIASPPRDHVFOVNNEALKT 180
Db 121 DSIDVKDPMADAGIIRYATGVLAQNRMNSKELNDASKPSQEHIKFVDEDALKD 180
Qy 181 IONOLRE 187
Db 181 IONOLKE 187

RESULT 6

Qy 121 DPLGKEDVPEADRGVTVYIGDARSKRSRQLNTIASPPRDHVFOVNNEALKT 180
Db 121 DSIDVKDPMADAGIIRYATGVLAQNRMNSKELNDASKPSQEHIKFVDEDALKD 180
Qy 181 IONOLRE 187
Db 181 IONOLKE 187

Query Match 29.71; Score 286.5; DB 15; Length 183;
US-10-346-863-33 Application US/10346863
; Sequence 33, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHILIPS, CHRISTOPHER BENJAMIN
; APPLICANT: PAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADMISSION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346, 863
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0019326, 3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447, 4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 33
; LENGTH: 182
; TYPE: PPT
; ORGANISM: Homo sapiens
; US-10-346-863-33

Query Match 29.71; Score 286.5; DB 15; Length 182;
US-10-346-863-33 Application US/10346863
; Sequence 33, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHILIPS, CHRISTOPHER BENJAMIN
; APPLICANT: PAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADMISSION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346, 863
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0019326, 3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447, 4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 33
; LENGTH: 182
; TYPE: PPT
; ORGANISM: Homo sapiens
; US-10-346-863-33

Query Match 29.71; Score 286.5; DB 15; Length 183;
US-10-346-863-33 Application US/10346863
; Sequence 33, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHILIPS, CHRISTOPHER BENJAMIN
; APPLICANT: PAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADMISSION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346, 863
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0019326, 3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447, 4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 20
; LENGTH: 183
; TYPE: PPT
; ORGANISM: Homo sapiens
; US-10-346-863-33

Query Match 29.71; Score 286.5; DB 15; Length 183;

Best Local Similarity 33.5%; Pred. No. 4e-22; Mismatches 67; Indels 7; Gaps 2;
Matches 61; Conservative 47; Miomatches 67; Score 286.5; DB 15; Length 183;
Organism: Homo sapiens US-10-346-663-41

Query Match 29.7%; Score 286.5; DB 16; Length 183;
Best Local Similarity 33.5%; Pred. No. 4e-22; Mismatches 67; Indels 7; Gaps 2;
Matches 61; Conservative 47; Miomatches 67; Score 286.5; DB 15; Length 183;
Organism: Homo sapiens US-10-346-663-41

RESULT 8
Sequence 41; Application US/10346863
Publication No. US20040103815A1
GENERAL INFORMATION
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: FAGAN, RICHARD JOSEPH
APPLICANT: PAGAN, RICHARD JOSEPH
TITLE OF INVENTION: ADHESION MOLECULES
FILE REFERENCE: 674575-2001
CURRENT APPLICATION NUMBER: US 10/346,863
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: PCT/GB01/03318
PRIOR FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: GB 0018126.3
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: GB 0025447.4
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 57
SEQUENCE ID NO: 11
LENGTH: 133
TYPE: PT
ORGANISM: Homo sapiens US-10-346-663-41

Query Match 29.7%; Score 286.5; DB 15; Length 183;
Best Local Similarity 33.5%; Pred. No. 4e-22; Mismatches 67; Indels 7; Gaps 2;
Matches 61; Conservative 47; Miomatches 67; Score 286.5; DB 15; Length 183;
Organism: Homo sapiens US-10-346-663-41

Query Match 29.7%; Score 286.5; DB 10; Length 184;
Best Local Similarity 33.0%; Pred. No. 4.e-22; Mismatches 70; Indels 7; Gaps 2;
Matches 62; Conservative 49; Miomatches 62; Score 286.5; DB 15; Length 184;
Organism: Homo sapiens US-09-805-354-4

RESULT 9
Sequence 7; Application US/10615515
Publication No. US2004011294A1
GENERAL INFORMATION
APPLICANT: FAGAN, RICHARD JOSEPH

DB 61 DYVKWDPOALLKAYRNLLTTGQINTVATEFRELGARDPDKYLLITGG--A 119
 Qy 121 DPLQSYEDVPRADRGCHCIVRIVGVDAPRSKSRQLNTASKPRDHYVPOVNNEALKT 180
 DB 119 TDSGNIDAKO-----IRVILIGKHFQTKESQETLHKSPKASPEVKILDPEKLD 173
 Qy 181 1QNLREK 188
 Db 174 LFTSLRK 181

RESULT 11
US-09-795-798-7
 Sequence 7, Application US/03795798
 Publication No. US20030107336A1
GENERAL INFORMATION:
 APPLICANT: Prestia, Leonard G.
 Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 NUMBER OF SEQUENCE: 24
CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Minirat (Genemethic)
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/795,798
 FILING DATE: 28-Feb-2001
 CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/974,899
 FILING DATE: Unknown
ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,376
 REFERENCE/DOCKET NUMBER: P014R1
TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: Amino Acid
 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-795-798-7

Query Match 29/31; Score 286.5; DB 10; Length 184;
 Best Local Similarity 33.8%; Pred. No. 4.1e-22; Mismatches 67; Indels 7; Gaps 2;
 Matches 61; Conservative 47; Mismatches 67; Indels 7; Gaps 2;

Qy	7 DIAFLDGSGLIPDHPRMKBFYSTMQLQKSKTFLSMQYSEFRHPTKEFQNNP 66	67 NPPSLVKEPTOLIGRHTATGKRVWELPNITNGARKNFKLIVVYTDGEKFDPGLYS 126
Db	5 DLVFLDGSGLIPDHPRMKBFYSTMQLQKSKTFLSMQYSEFRHPTKEFQNNP 66	65 DDALDGHKHMULLNGMINTGAQVNTVATEFRELGARDPDKYLLITGG--ATDSGNI 122
Qy	127 DPLQSAEDEVTVYGVGDAPRSKSRQLNTASKPRDHYVPOVNNEALKT 186	123 DAKO-----IRVILIGKHFQTKESQETLHKSPKASPEVKILDPEKLD 177
Db	187 EK 188	174 LFTSLRK 179

RESULT 12	US-09-758-493-4	Sequence 4, Application US/09758493 Publication No. US0040086335A1 GENERAL INFORMATION: APPLICANT: Arnalout, M. Amin Li, Rui APPLICANT: Xiong, Jian-Ping TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND TITLES THEREOF FILE REFERENCE: 00786-004001 CURRENT FILING DATE: US/09/758,493 PRIORITY APPLICATION NUMBER: US 60/221, 950 PRIOR FILING DATE: 2000-07-31 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Fast-SEQ for Windows Version 4.0 SEQ ID NO: 4 TYPE: PRT ORGANISM: Homo sapiens
RESULTS 13	US-09-758-493-4	Query Match Score 2971; DB 11; Length 29 Best Local Similarity 33.0%; Pred. No. 4.1e-22; Matches 62; Conservative 49; Mismatches 70; Indels 18
DY	1 CPQDSDIAFLDGSGS1PHDFRMRKSTV5MBQLSKTSKTLFSMOM 1 CIRKNNDVPLDGMSLQSPDEQKILDFMDVKNNKLSNTSFOAVPKF 1 BQPNQNPNSLKVPTQLGRITATGKRVRELFTINGARKHAFKI 1 DYKMKDPLAKVFMKLMLTTGKA INVATYVFRBEGLRPAKIV 121 DPGYSDVTPEDRGVTRVTCGDAFRSKSROELNTIASKPPRDY 61 TDSQNDAAKD----TIRVIGKHFQTKESQETLHKPASKPASEFV 119 1QNLQEK 188 174 LTFEQKK 181	Query Match Score 2865; DB 11; Length 29 Best Local Similarity 33.0%; Pred. No. 4.1e-22; Matches 62; Conservative 49; Mismatches 70; Indels 18
DY	1 CIRKNNDVPLDGMSLQSPDEQKILDFMDVKNNKLSNTSFOAVPKF 1 BQPNQNPNSLKVPTQLGRITATGKRVRELFTINGARKHAFKI 1 DYKMKDPLAKVFMKLMLTTGKA INVATYVFRBEGLRPAKIV 121 DPGYSDVTPEDRGVTRVTCGDAFRSKSROELNTIASKPPRDY 61 TDSQNDAAKD----TIRVIGKHFQTKESQETLHKPASKPASEFV 119 1QNLQEK 188 174 LTFEQKK 181	Query Match Score 2865; DB 11; Length 29 Best Local Similarity 33.0%; Pred. No. 4.1e-22; Matches 62; Conservative 49; Mismatches 70; Indels 18
RESULTS 13	US-09-758-493-4	Query Match Score 2971; DB 14; Length 29 Best Local Similarity 33.0%; Pred. No. 4.1e-22; Matches 62; Conservative 49; Mismatches 70; Indels 18
DY	1 Sequence 4, Application US/10144259 GENERAL INFORMATION: APPLICANT: Arnalout, M. Amin Li, Rui APPLICANT: Xiong, Jian-Ping TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF FILE REFERENCE: 00786-548001 CURRENT APPLICATION NUMBER: US/10/144,259 CURRENT FILING DATE: 2002-09-04 PRIOR APPLICATION NUMBER: US 09/758,493 PRIOR FILING DATE: 2000-01-11 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Fast-SEQ for Windows Version 4.0 SEQ ID NO: 4 TYPE: PRT ORGANISM: Homo sapiens	Query Match Score 2971; DB 14; Length 29 Best Local Similarity 33.0%; Pred. No. 4.1e-22; Matches 62; Conservative 49; Mismatches 70; Indels 18

RESULT 15
US-10-727-737-7 ; Sequence 7, Application US/10727737
; Publication No. US20040146507A1

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- BLACK BORDERS**
- IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- FADED TEXT OR DRAWING**
- BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- SKEWED/SLANTED IMAGES**
- COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- GRAY SCALE DOCUMENTS**
- LINES OR MARKS ON ORIGINAL DOCUMENT**
- REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- OTHER:** _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.